

Qy 1384 AGTGGAGATGAAGATGGAGAAGATCCAGACAAGAGAATTCTATTGAGCATCAGACAAG 1443
 Db 462 SerGlyAspGluAspGlyGluAspProAspLysArgIleSerIleArgAlaSerAspLys 481

Qy 1444 CGGATAGCTTGTGATGAAGAATTCTCAGATTCTGAGGATGAAGGAGAAGGAGGTCGAAGA 1503
 Db 482 ArgIleAlaCysAspGluGluPheSerAspSerGluAspGluGlyGluGlyGlyArgArg 501

Qy 1504 AATGTGGCTGATCATAAGAAACGGAGCAAGAAAGCTAGAATTGAAGAAGATAAGAAAGAA 1563
 Db 502 AsnValAlaAspHisLysLysGlyAlaLysIysAlaArgIleGluGluAspLysGlu 521

Qy 1564 ACAGAGGACAAAAACAGACGTTAAGGAAGAAGATAATCCAAGGACAACAGTGGTGAA 1623
 Db 522 ThrGluAspLysLysThrAspValLysGluGluAspLysSerLysAspAsnSerGlyGlu 541

Qy 1624 AAAACAGATAACCAAGGAACCAAATCAGAACAGCTCAGCAACCCC 1668
 Db 542 LysThrAspThrLysGlyThrLysSerGluGlnLeuSerAsnPro 556

RESULT 2

AAB49955

ID AAB49955 standard; protein; 488 AA.

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AC AAB49955;

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DT 08-MAR-2001 (first entry)

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DE Human histone deacetylase HDAC-2.

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KW Histone deacetylase; HDAC-1; HDAC-2; HDAC-3; HDAC-4; HDAC-5; HDAC-C; HDAC-D; cell cycle; tumourigenesis; cancer; inhibitor; antisense; gene therapy.

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OS Homo sapiens.

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PN WO200071703-A2.

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PD 30-NOV-2000.

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PF 03-MAY-2000; 2000WO-IB001252.

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PR 03-MAY-1999; 99US-0132287P.

XX

PA (METH-) METHYLGENE INC.

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PI Macleod AR, Li Z, Besterman JM;

XX

DR WPI; 2001-016407/02.

DR N-PSDB; AAC89555.

XX

PT Antisense oligonucleotide that inhibits expression of a histone deacetylase, useful for treating and/or alleviating the symptoms of neoplasia, or for inhibiting neoplastic cell growth in an animal.

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PS Disclosure; Page 51-53; 125pp; English.

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CC The present invention provides inhibitors of histone deacetylase enzymes such as HDAC-1, HDAC-2, HDAC-3, HDAC-4, HDAC-5, HDAC-C and HDAC-D. These inhibitors may be antisense strands or they may be compounds identified

CC by contacting the enzyme with the compound and measuring the resulting
 CC enzyme activity. These inhibitors are useful for treating cancers and for
 CC identifying which histone deacetylase is involved in a neoplasia
 XX
 SQ Sequence 488 AA;

Alignment Scores:

Pred. No.:	4.1e-248	Length:	488
Score:	2636.00	Matches:	488
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	74.5%	Indels:	0
DB:	4	Gaps:	0

US-10-528-104-5 (1-1985) x AAB49955 (1-488)

Qy	205	ATGGCGTACAGTCAAGGAGGCGGCAAAAAAAAGTCTGCTACTACTACGACGGTGATATT	264
Db	1	MetAlaTyrSerGlnGlyGlyLysLysLysValCysTyrTyrTyrAspGlyAspIle	20
Qy	265	GGAAATTATTATTATGGACAGGGTCATCCCATGAAGCCTCATAGAATCCGCATGACCCAT	324
Db	21	GlyAsnTyrTyrTyrGlyGlnGlyHisProMetLysProHisArgIleArgMetThrHis	40
Qy	325	AACTTGCTGTTAATTATGGCTTACAGAAAAATGGAAATATATAGGCCCATAAAGCC	384
Db	41	AsnLeuLeuLeuAsnTyrGlyLeuTyrArgLysMetGluIleTyrArgProHisLysAla	60
Qy	385	ACTGCCGAAGAAAATGACAAAATATCACAGTGATGAGTATATCAAATTCTACGGTCAATA	444
Db	61	ThrAlaGluGluMetThrLysTyrHisSerAspGluTyrIleLysPheLeuArgSerIle	80
Qy	445	AGACCAGATAACATGTCAGTGAGTATAGTAAGCAGATGCATATATTAAATTGTTGGAGAAGAT	504
Db	81	ArgProAspAsnMetSerGluTyrSerLysGlnMetHisIlePheAsnValGlyGluAsp	100
Qy	505	TGTCCAGCGTTGATGGACTCTTGAGTTGTCAGCTCTCAACTGGCGGTTCAGTGCT	564
Db	101	CysProAlaPheAspGlyLeuPheGluPheCysGlnLeuSerThrGlyGlySerValAla	120
Qy	565	GGAGCTGTGAAGTAAACCGACAACAGACTGATATGGCTGTTAATTGGGCTGGAGGATTA	624
Db	121	GlyAlaValLysLeuAsnArgGlnGlnThrAspMetAlaValAsnTrpAlaGlyGlyLeu	140
Qy	625	CATCATGCTAAGAAATACGAAGCATCAGGATTCTGTTACGTTAATGATATTGTGCTGCC	684
Db	141	HisHisAlaLysLysTyrGluAlaSerGlyPheCysTyrValAsnAspIleValLeuAla	160
Qy	685	ATCCTTGAATTACTAAAGTATCATCAGAGAGCTTATATATTGATATAGATATTGATCAT	744
Db	161	IleLeuGluLeuLysTyrHisGlnArgValLeuTyrIleAspIleAspIleHisHis	180
Qy	745	GGTGTGGTGTGAAAGAAGCTTTTATACAAACAGATCGTGTAAATGACGGTATCATTCCAT	804
Db	181	GlyAspGlyValGluGluAlaPheTyrThrAspArgValMetThrValSerPheHis	200
Qy	805	AAATATGGGAATACTTCTGGCACAGGAGACTTGAGGGATATTGGTGCTGGAAAGGC	864
Db	201	LysTyrGlyGluTyrPheProGlyThrGlyAspLeuArgAspIleGlyAlaGlyLysGly	220
Qy	865	AAATACTATGCTGTCAATTCCAATGTGTGATGGTATAGATGATGAGTCATATGGCAG	924

Db	221	LysTyrTyrAlaValAsnPheProMetCysAspGlyIleAspAspGluSerTyrGlyGln	240
Qy	925	ATATTAAAGCCTATTATCTCAAAGGTGATGGAGATGTATCAACCTAGTGTGGTATTA	984
Db	241	IlePheLysProIleIleSerLysValMetGluMetTyrGlnProSerAlaValLeu	260
Qy	985	CAGTGTGGTGCAGACTCATTATCTGGTGTAGACTGGGTTGTTCAATCTAACAGTC	1044
Db	261	GlnCysGlyAlaAspSerLeuSerGlyAspArgLeuGlyCysPheAsnLeuThrValLys	280
Qy	1045	GGTCATGCTAAATGTGTAGAAGTTGTAAGAACTTTAACCTTACCAATTACTGATGCTTG	1104
Db	281	GlyHisAlaLysCysValGluValValLysThrPheAsnLeuProLeuLeuMetLeuGly	300
Qy	1105	GGAGGTGGCTACACAATCCGTAAATGTTGCTCGATGTTGGACATATGAGACTGCAGTG	1164
Db	301	GlyGlyGlyTyrThrIleArgAsnValAlaArgCysTrpThrTyrGluThrAlaValAla	320
Qy	1165	CTTGATTGTGAGATTCCCAATGAGTTGCCATATAATGATTACTTGAGTATTTGGACCA	1224
Db	321	LeuAspCysGluIleProAsnGluLeuProTyrAsnAspTyrPheGluTyrPheGlyPro	340
Qy	1225	GACTTCAAACACTGCATATTAGCCTTCAAACATGACAAACCAGAACACTCCAGAATATG	1284
Db	341	AspPheLysLeuHisIleSerProSerAsnMetThrAsnGlnAsnThrProGluTyrMet	360
Qy	1285	GAAAAGATAAAACAGCGTTGTTGAAAATTGCGCATGTTACCTCATGCACCTGGTG	1344
Db	361	GluLysIleLysGlnArgLeuPheGluAsnLeuArgMetLeuProHisAlaProGlyVal	380
Qy	1345	CAGATGCAAGCTATTCCAGAAGATGCTGTTCATGAAGACAGTGGAGATGAAGATGGAGA	1404
Db	381	GlnMetGlnAlaIleProGluAspAlaValHisGluAspSerGlyAspGluAspGlyGlu	400
Qy	1405	GATCCAGACAAGAGAATTCTATTGAGCAGACAGCAGGATAGCTTGTGATGAAGAA	1464
Db	401	AspProAspLysArgIleSerIleArgAlaSerAspLysArgIleAlaCysAspGluGlu	420
Qy	1465	TTCTCAGATTCTGAGGATGAAGGAGAAGGGAGGTCGAAGAAATGTGGCTGATCATAAGAAA	1524
Db	421	PheSerAspSerGluAspGluGlyGluGlyArgArgAsnValAlaAspHisLysLys	440
Qy	1525	GGAGCAAAGAAAGCTAGAATTGAAGAAGATAAGAAAGAACAGAGGACAAAAACAGAC	1584
Db	441	GlyAlaLysLysAlaArgIleGluGluAspLysLysGluThrGluAspLysLysThrAsp	460
Qy	1585	GTAAAGGAAGATAAAATCCAAGGACAACAGTGGTAAAAAACAGATAACCAAAGGAACC	1644
Db	461	ValLysGluGluAspLysSerLysAspAsnSerGlyGluLysThrAspThrLysGlyThr	480
Qy	1645	AAATCAGAACAGCTCAGCAACCCC	1668
Db	481	LysSerGluGlnLeuSerAsnPro	488

RESULT 3

ABR47485

ID ABR47485 standard; protein; 488 AA.

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AC ABR47485;

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